Patent
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Serial No.: 10/763,810	)	Examiner: LAM, Ann Y.
	)	
Filed: January 23, 2004	)	Confirmation No.: 5010
	)	
Title: **DETECTION OF BINDING SPECIES WITH COLLOIDAL AND NON-COLLOIDAL STRUCTURES**	)	

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Commissioner for Patents
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AMENDMENT UNDER 37 C.F.R. § 1.114

Sir:

In response to the Office Action dated February 18, 2010, in connection with the above-identified application, please enter and consider the following amendment and remarks.

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application. Canceled claims have been canceled without prejudice.

Listing of Claims:

1-120. (Canceled)

121. (Previously presented) A method of determining interactive characteristics of a sample component comprising:

exposing at least two surface regions, each presenting a different chemical, biochemical, or biological functionality, to a sample;

determining an interaction pattern of the sample with the at least two surface regions on the surface, indicative of an interaction characteristic between at least one component of the sample with the at least two surface regions.

122. (Previously presented) The method according to claim 121, wherein the sample includes at least two components that carry, or are adapted to carry, identical immobilized signaling entities, and/or the determining step is carried out without determining the identity of the at least one component after interaction with the at least two surface regions.

123. (Previously presented) The method according to claim 121, comprising:

presenting at least three surface regions, each exposing a different chemical, biochemical, or biological functionality;

exposing the at least three surface regions to the sample; and

determining an interaction pattern of the sample with the at least three surface regions, indicative of an interaction characteristic between at least two components of the sample with each of the at least three surface regions, preferably wherein each of at least two of the at least three components becomes immobilized at a surface region, indicative of the interaction pattern.

124. (Previously presented) The method according to claim 123, wherein the sample is a first sample, further comprising exposing at least three surface regions, each exposing a different chemical, biochemical, or biological functionality, to a second sample;

determining an interaction pattern of the second sample with the at least three surface regions to which the second sample has been exposed, indicative of an interaction characteristic between at least two components of the second sample with each of the at least three surface regions; and

comparing the interaction pattern of the second sample with the interaction pattern of the first sample.

125. (Previously presented) The method according to claim 124, comprising exposing the second sample to a third sample, prior to exposing the second sample to the at least three surface regions, and comparing the interaction pattern of the second sample to the interaction pattern generated when the second sample has not been pre-exposed to the third sample.

126. (Previously presented) The method according to claim 125, wherein the third sample is a drug or a drug candidate.

127. (Previously presented) The method according to claim 125, wherein the second sample comprises a plurality of different species.

128. (Previously presented) The method according to claim 127, wherein the second sample comprises products of a cDNA library.

129. (Previously presented) The method according to claim 124, wherein:

a) the at least three surface regions to which the first sample is exposed are essentially identical to the at least three surface regions to which the second sample is exposed; or

b) each of the at least three surface regions to which the second sample is exposed is arranged to correspond to one of the at least three surface regions to which the first sample was exposed; or

c) at least one of the first sample and second sample is derived from proteins, known drugs, putative drugs, cell lysates, cDNA libraries or their products, natural products and mixtures thereof, preferably wherein:

i) at least one of the first sample and second sample is a cell lysate from a cell that has been treated with a drug or putative drug; or

ii) the interaction pattern is determined by detecting a signal at or near each of the at least two surface regions, preferably wherein the signal is light emission or electrical; or

d) the interaction pattern is determined by surface plasmon resonance (SPR) or quartz crystal microbalance (QCM).

130. (Previously presented) The method according to claim 121, wherein:

a) the sample is selected from known drugs, putative drugs, cell lysates, cDNA libraries or their products, natural products and mixtures thereof, preferably wherein the sample has been exposed to a drug or putative drug; or

b) the interaction pattern is determined by:

i) detecting a signal at the at least two surface regions, preferably wherein the signal is light emission or electrical; or

ii) QCM or SPR; or

c) said method further comprises comparing the interaction pattern to a library of known interaction patterns; or

d) wherein at least one of the two surface regions presents a protein, nucleic acid, peptide, drug, small molecule or a mixture thereof; or

e) said method further comprises immobilizing a colloid to a component of the sample.

131. (Previously presented) The method according to claim 122, comprising:

exposing at least ten surface regions, each presenting a different chemical, biochemical, or biological functionality to a sample containing at least ten components;

determining an interaction pattern of the sample with the at least ten surface regions, indicative of an interaction characteristic between at least ten components of the sample with the at least ten surface regions;

wherein the at least ten components of the sample carry, or are adapted to carry, identical immobilized signaling entities, and/or the determining step is carried out without determining the identity of at least one of the at least ten components after interaction with the at least two surface regions, preferably wherein the determining step is carried out without determining the identity of any of the at least ten components after interaction with the at least two surface regions.

REMARKS

Claims 121-131 are pending in the application. No new matter has been inserted into the application.

Rejection Under 35 U.S.C. §102(e) Over Li '104 (US 6,704,104)

Claims 121, 122 and 130 have been rejected under 35 U.S.C. §102(e) as being anticipated by Li '104. Applicant traverses this rejection. Reconsideration and withdrawal thereof are respectfully requested.

The Examiner is reminded that in order to establish *prima facie* anticipation, each and every limitation of the presently claimed invention must be disclosed in the cited reference.

The presently claimed invention is directed to a method of determining interactive characteristics of a sample component comprising: exposing at least two surface regions, each presenting a different chemical, biochemical, or biological functionality, to a sample; and determining an interaction pattern of the sample with the at least two surface regions on the surface, indicative of an interaction characteristic between at least one component of the sample with the at least two surface regions.

Li '104

Li '104 discloses an array detector making a spatially addressable array of various biological species. In particular, Li '104 discloses immobilizing DNA at different sites. Li '104 discloses that the biological species deposited at each site of the array is previously known. Thus, Li '104 discloses an array detector that can sensitively detect each location of a high density DNA array.

In contrast to Li '104, the presently claimed inventive subject matter is directed to the concept of compound "fingerprinting". Unknown drug candidates may be characterized from protein binding modules per array. Without limitation, the invention may be envisioned in the following way.

An array of protein modules or protein motifs is formed. A cDNA library which may produce about 30,000 gene products may be recombinantly engineered to express histidine, maybe 6 or 7 histidine residues at the C terminal end. These expressed proteins may be mixed

with the array and may bind some of the proteins. Some of these proteins may bind to particular motifs at a particular locus.

The result is the creation of an intensity topography. For example, a nanoparticle bearing a nickel-NTA with a signal is added to bind to the bound proteins. This sort of a fingerprint is useful for instance, in taking a cDNA library from the heart tissue for instance, in which the proteins that are expressed in the heart can be bound to this array and the heart's protein fingerprint can be obtained.

Drug intervention resulting in the intervention of binding between the protein and the module can be assayed, which results in a particular type of topography and fingerprint for the protein obtained from a particular tissue. Therefore, a drug profile can be obtained for its effect or side-effects on the heart or kidney or any other organ by comparing a potentially new drug and its effect on the heart to see if an established effect of a drug on the protein profile can be matched to such a "fingerprint". If there is toxic effect of the drug in the established drug, then a decision can be used to not use it for its toxicity.

Therefore, in contrast to Li '104 the presently claimed invention is directed to detecting the interactants' activities and patterns on the surface where the interaction takes place, which presents its own set of advantages and efficiency for fingerprinting. Accordingly, Li '104 fails to anticipate the presently claimed invention.

Rejection Under 35 U.S.C. §103(a) Over Li '104 (US 6,704,104)

Claims 123-129 and 131 have been rejected under 35 U.S.C. §103(a) as being "obvious" over Li '104. Applicant traverses this rejection. Reconsideration and withdrawal thereof are respectfully requested.

Li '104 is described above.

Given that Li '104 discloses an array detector making a spatially addressable array of various biological species. In particular, Li '104 discloses an array detector that can sensitively detect each location of a high density DNA array, and since Li '104 fails to disclose any pattern formation or "fingerprinting" aspect of the claimed invention, the Li '104 reference cannot be

said to render the claimed invention obvious. Accordingly, the presently claimed invention is patentable over the cited reference.

Conclusion

It is believed that the application is now in condition for allowance. Applicants request the Examiner to issue a notice of Allowance in due course. The Examiner is encouraged to contact the undersigned to further the prosecution of the present invention.

The Commissioner is authorized to charge JHK Law's Deposit Account No. **502486** for any fees required under 37 CFR § 1.16 and 1.17 and to credit any overpayment to said Deposit Account No. **502486**.

Respectfully submitted,

JHK Law

Dated: October 27, 2011

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